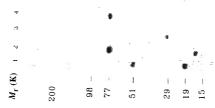




CONSTRUCTOR CONSTRUCTOR



2/6

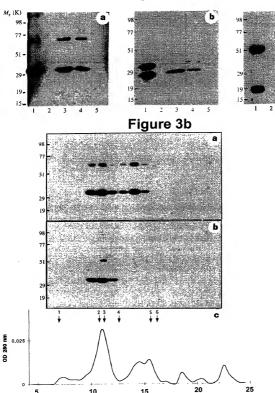
Figure 2

| MASP-2 | Clr/Cls> | |
|--------|---|-----|
| | TPLGPKWPEPVFGRLASPGFPGEYANDQERRWTLTAPPGYRLRLYFTHFDLELSHL@EYDFVKLSSGAKVLATL@GQESTDTERAPGKDT | 90 |
| MASP-1 | HTVELNNMFGQIQSPGYPDSYPSDSEVTWNITVPDGFRIKLYFMHFNLESSYLGEYDYVKVETEDQVLATF@GRETTDTEQTPGQEV | 87 |
| Clr | SIPIPQKLFGEVTSPLFPKPYPNNFETTTVITVPTGYRVKLVFQQFDLEPSEGÇFYDYVKISADKKSLGRFÖGQLGSPLGNPPGKKE | 87 |
| Cls | EPTMYGEILSPNYPQAYPSEVEKSWDIEVPEGYGIHLYFTHLDIELSENÇAYDSVQIISGDTEEGRLÇGQRSSNNPHSPIVEE | 83 |
| | * ** * * * * * * * * * * * * * * * * * * | |
| MASP-2 | FY <u>SLGSSLDITFRSDYSNEKP</u> <u>FTGFEAFY</u> AAEDIDEÇQ VAPGEA PTĞDHHĞHNHLGGFYĞSĞRAGYVLHRNKRTĞSALĞS | 170 |
| MASP-1 | VLSPGSFMSITFRSDFSNEER FTGFDAHYMAVDVDECK EREDEE LSCDHYCHNYIGGYYCSCRFGYILHTDNRTCRVECS | 167 |
| Clr | FMSQGNKMLLTFHTDFSNEENGTIMFYKGFLAYYQAVDLDEĞASRSKSGEEDPOPOĞOHLĞHNYVGGYFĞSĞRPGYELOEDRHSĞOABĞS | 177 |
| Cls | FOVPYNKLOVIFKSDFSNEER FTGFAAYYVATDINECT DFVD VPCSHFCNNFIGGYFCSCPPEYFLHDDMKNCGVNCS | 161 |
| | ************************************** | 101 |
| | - Clr/Cls> | |
| MASP-2 | GOVFTORSGELSSPEYPRPYPKLSSÖTYSISLBEGFSVILDFV ESFDVET HPETLØPYDFLKIQTDREEHGPFØGKTLPHR IETKS | 256 |
| MASP-1 | DNLFTQRTGVITSPDFPNPYPKSSBÖLYTIELEEGFMVNLQFB DIFDIED HPBVPÖPYDYIKIKVGPKVLGPFÖGEKAPEP ISTQS | 253 |
| Clr | SELYTEASGYISSLEYPRSYPPDLRCNYSIRVERGLTLHLKFL EPFDIDD HQQVHCPYDQLQIYANGKNIGEFCGKQRPPD LDTSS | 263 |
| Cls | gdvftaligeiaspnypkpypensræeyqirlekgfqvvvtlrredfdveaadsagnældslvfvagdrqfgpy&ghgfpgplnietks | 250 |
| | · · · · · · · · · · · · · · · · · · · | |
| | CCP-1> | |
| MASP-2 | | 345 |
| MASP-1 | | 342 |
| Clr | | 353 |
| Cls | naldiifqtdltgqkkgwklryhgdpmpgpkedtpn svwepakakyvfrdvvqitgldgfevvegrvgatsfystgqsngkwsnsklk | 338 |
| | | |
| WASP-2 | CCP-2> ESIVDÖGPPDDLPSGRVEYITGPGVTTYKAVIOYSÖEBTFYTM KVNDGKYVÖBADGFWTSSKGEKSLPVÖBPVÖGLS ARTT | 426 |
| MASP-1 | CKIVDCRAPGELEHGLITFSTRNNLTTYKSEIKYSCOEPYYKML NNNTGIYTCSACGVWMNKVLGRSLPTCLPVCGLPKPSRKL | 426 |
| Cir | ËKIKDËGQPRNLPNGDFRYTTTMGVNTYKARIQYYËHEPYYKMOTRAGSRESEOGVYTËTAQGIWKNEOKGEKIPRËLPVËGKPVNPVEO | 443 |
| Cls | COPYDCGIPESIENGKVE DPESTLFGSVIRYTCEEPYYYME NGGGGEYHCAGNGSWYNEVLGPELPKCYPYCGYPREPFRE | 419 |
| | * | 417 |
| | —— serine protesse —→> ∇ | |
| MASP-2 | GGRIYGGGKAKGGFPWOVILIGGTTA AGALLYDNWVLTAAH AVYEOKHDASALDIRMGTLKRLSPHYTOAWSEAVFIHEG | 507 |
| MASP-1 | MARIFNGRPAQKGTTPWIAMLSHLNGQPFCGGSLLGSSWIVTAAHCLHOSLDPKDPTLRDSDLLSPSD FKIILGKHWRLRSDENEOHLG | 515 |
| Clr | RQRIIGGQKAKMGNFPWOVFTNIHGRG GGALLGDRWILTAAH TLYPKEHEAOSNASLDVFLGHTNVEELMKLGNHP IRRV | 523 |
| Cls | KQRIIGGSDADIKNFPWQVFFDNPWA GGALINEYWVLTAAH VVEGNREPTMYVGSTSVOTSRLAKSKMLT PEHVFIHPG | 498 |
| | ** * * * ** | |
| | > | |
| MASP-2 | YTHDAG FDNDIALIKLNNKVVINSNITPIĞLPRKEAESFMRTDDIGTASGWGLTQRGFLARNLMYVDIPIVDHQKQTAAYEK | 589 |
| MASP-1 | VKHTTLHPKYDPNTFENDVALVELLESPVLNAFVMPIÄLP EGPQQEGAMVIVSGWGKQFLQRFPETLMEIEIPIVDHSTÄQKAY | 599 |
| Clr | SVHPDYRQDESYN FEGDIALLELENSVTLGPNLLPIGLP DNDTFYDLGLMGYVSGFGVMEEK IAHDLRFVRLPVANPQAGEN WLR | 608 |
| Cls | WKLLEV PEGRTN FDNDIALVRLKDPVKMGPTVSPIČLPGTSSDYNLMDGDLGLISGWGRTEKRDRAVRLKAARLPVAPLRKCKEVKVE | 586 |
| | * | |
| | . • | |
| MASP-2 | PPYPRG SVTANMLÇAGLESGGKDSÇRGDSGGALVFLDS ETERWFVGGIVSWGSMNKGEAGQYGVYTKVINYIPWIENIISDF | 671 |
| MASP-1 | APLKK KVTRDMIĞAGBKEGGKDAĞSGDFMVTLNR ERGQWYLVGTVSWGD DĞCKKDRYGVYSYIHHNKDWIQRVTGVRN | 680 |
| Cir | GKNRMD VFSQNMFÇAGHPSLKQDAÇQGDSGGVFAVRDP NTDRWVATGIVSWGI GÇSRG YGFYTKVLNYVDWIKKEMBEED | 688 |
| Cls | KPTADAEAYVFTPNMICAGGEK GMDSCKGDSGGAFAVQDPNDKTKFYAAGLVSWGP QCGT YGLYTRVKNYVDWIMKTMOENSTPRED | 673 |

3/6 Figure 3a

10

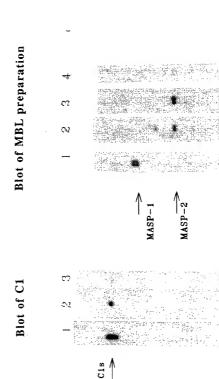
COMPAND MATACOC



15

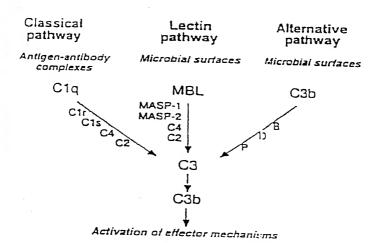
Figure 4

COMPAND. DURCH



5/6

Figure 5



6/6

Figure 6

